

O 500 #4  
OIPE CWS  
4501

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/724,915  
 DATE: 12/14/2000  
 TIME: 09:22:49

**ENTERED**

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3 <110> APPLICANT: Nakayama, Naoki  
 4 Wen, Duanzhi  
 5 Han, Chun-ya  
 6 He, Ching  
 7 Yu, Dongyin  
 9 <120> TITLE OF INVENTION: Chordin-like Molecules and Uses Thereof  
 11 <130> FILE REFERENCE: 99,569-A  
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/724,915  
 C--> 14 <141> CURRENT FILING DATE: 2000-11-28  
 16 <150> PRIOR APPLICATION NUMBER: 60/169,494  
 17 <151> PRIOR FILING DATE: 1999-12-07  
 19 <160> NUMBER OF SEQ ID NOS: 37  
 21 <170> SOFTWARE: PatentIn Ver. 2.0  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1864  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Mus musculus  
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 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (148)..(1146)  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: sig\_peptide  
 34 <222> LOCATION: (148)..(213)  
 36 <400> SEQUENCE: 1  
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 39 gccagtgccc agcttttagtc caccgctcct ctcccttgag ccctgaatt gcattttgca 120  
 41 gtagctcgaa ggagaaaaaa gtagaag atg gat ggc atg aaa tac atc att tcc 174  
 42 Met Asp Gly Met Lys Tyr Ile Ile Ser  
 43 1 5  
 45 tta ttt ttc atc ttt gtt ttc cta gaa gga agc aaa aca gaa caa gta 222  
 46 Leu Phe Phe Ile Phe Val Phe Leu Glu Gly Ser Lys Thr Glu Gln Val  
 47 10 15 20 25  
 49 aaa cac tca gac aca tat tgc gtg ttt caa gac aag aag tat aga gtg 270  
 50 Lys His Ser Asp Thr Tyr Cys Val Phe Gln Asp Lys Lys Tyr Arg Val  
 51 30 35 40  
 53 ggt gag aaa tgg cat ccc tac ctg gaa ccg tat gga ctg gtt tac tgt 318  
 54 Gly Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys  
 55 45 50 55  
 57 gtg aac tgc atc tgc tct gag aat ggg aat gtg ctt tgc agc cga gtc 366  
 58 Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val  
 59 60 65 70  
 61 aga tgt cca agt ctt cat tgc ctt tca ccc gtg cat att cct cat ctc 414  
 62 Arg Cys Pro Ser Leu His Cys Leu Ser Pro Val His Ile Pro His Leu  
 63 75 80 85  
 65 tgt tgc ccc cgc tgc cca gac tcc tta cca cca gtg aac aat aag gtg 462  
 66 Cys Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn Asn Lys Val  
 67 90 95 100 105

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70 Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu
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73 ctg ttc ata gct gaa ggg ctc ttt caq aac cgg caa ccc aat cag tgc 558
74 Leu Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys
75      125      130      135
77 agt caq tgt agc tgc tcg gag ggg aat gta tac tgt ggt ctc aag act 606
78 Ser Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr
79      140      145      150
81 tgc ccc aaa ctg acc tgt gca ttc cca gtc tct gtt cca gat tct tgc 654
82 Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys
83      155      160      165
85 tgc cga gta tgc aga ggg gat gca gaa tta tcg tgg gaa cat gcg gat 702
86 Cys Arg Val Cys Arg Gly Asp Ala Glu Leu Ser Trp Glu His Ala Asp
87 170      175      180      185
89 ggt gat atc ttc cgg caa cct gcc aac aga gaa gca aga cat tct tac 750
90 Gly Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg His Ser Tyr
91      190      195      200
93 ctc cgt tcc ccc tac gat cct cca cca aac aga caa gct gga ggt ctt 798
94 Leu Arg Ser Pro Tyr Asp Pro Pro Pro Asn Arg Gln Ala Gly Gly Leu
95      205      210      215
97 ccc cgc ttt cct ggg agc aga agt cac cgg gga gct gtt ata gat tcc 846
98 Pro Arg Phe Pro Gly Ser Arg Ser His Arg Gly Ala Val Ile Asp Ser
99      220      225      230
101 cag caa gca tcc ggg acc atc gtg cag att gtc atc aat aac aag cac 894
102 Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His
103      235      240      245
105 aaa cat gga caa gtg tgt gtt tcc aat gga aag acc tac tct cat gga 942
106 Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly
107 250      255      260      265
109 gag tcc tgg cac cca aat cta cga gca ttt ggc att gtg gaa tgt gta 990
110 Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val
111      270      275      280
113 cta tgc act tgt aat gtc acc aag caa gaa tgt aag aaa atc cac tgc 1038
114 Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys Ile His Cys
115      285      290      295
117 ccc aat cga tac ccc tgc aag tat cct caa aaa ata gat gga aag tgc 1086
118 Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys
119      300      305      310
121 tgc aag gtg tgc cca ggt aaa aag gca aaa ggt gca ttg gct gga ggc 1134
122 Cys Lys Val Cys Pro Gly Lys Lys Ala Lys Gly Ala Leu Ala Gly Gly
123      315      320      325
125 cct gcc ttt ggt tgaatgagat tcacacatag tccatttcag tcttctttgt 1186
126 Pro Ala Phe Gly
127 330
129 tcattcaaac tataaatgac ctgtcttata gttctaacga taatagtctt agcaagaatg 1246
131 aacttcattc ttctgtcttc tgagacactg atggttgctt tgaaggaatt aactactcag 1306
133 agtttctttt gttcacaatg tcaaacacat gccaaagtgc ttatcttggt ctgtcttttc 1366
135 taaattagag agtttactgt atcactgttt tagaaaaagt cacacctttc atggttttaa 1426

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Input Set : A:\99569Aseq.txt

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137 tcaccaactc acttcaagac ataatccagt actcttttca gatgagatat aaatgagtta 1486
139 cagtggagag aaattagatt ctgatccaaa tgcatacaat ccacaagtat cttaccccat 1546
141 qtgaacattt taaagtttat tactgtgttc cacattgcta ttttaatttg caatttcctt 1606
143 ttaaattttc tgagatattg tatctgtata tacttatggg gtacagtatg ttaattcaat 1666
145 acaaatatac aaggtataut tgcataatca gggtaattat cattctctct cctctgattr 1726
147 tateccataga ctcttctagt cattttaaaaa tttatcatca attgggtttt tgatatggta 1786
149 actccactgt gctaangaaa ccattcattc taatggcatt ttaggatcta ctatctaacc 1846
151 tctatctccc ctctgttt                                     1864
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 333
156 <212> TYPE: PRT
157 <213> ORGANISM: Mus musculus
159 <400> SEQUENCE: 2
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163 Leu Glu Gly Ser Lys Thr Glu Gln Val Lys His Ser Asp Thr Tyr Cys
164 20 25 30
166 Val Phe Gln Asp Lys Lys Tyr Arg Val Gly Glu Lys Trp His Pro Tyr
167 35 40 45
169 Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn Cys Ile Cys Ser Glu
170 50 55 60
172 Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys Pro Ser Leu His Cys
173 65 70 75 80
175 Leu Ser Pro Val His Ile Pro His Leu Cys Cys Pro Arg Cys Pro Asp
176 85 90 95
178 Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr
179 100 105 110
181 Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe Ile Ala Glu Gly Leu
182 115 120 125
184 Phe Gln Asn Arg Gln Pro Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu
185 130 135 140
187 Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala
188 145 150 155 160
190 Phe Pro Val Ser Val Pro Asp Ser Cys Cys Arg Val Cys Arg Gly Asp
191 165 170 175
193 Ala Glu Leu Ser Trp Glu His Ala Asp Gly Asp Ile Phe Arg Gln Pro
194 180 185 190
196 Ala Asn Arg Glu Ala Arg His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro
197 195 200 205
199 Pro Pro Asn Arg Gln Ala Gly Gly Leu Pro Arg Phe Pro Gly Ser Arg
200 210 215 220
202 Ser His Arg Gly Ala Val Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile
203 225 230 235 240
205 Val Gln Ile Val Ile Asn Asn Lys His Lys His Gly Gln Val Cys Val
206 245 250 255
208 Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser Trp His Pro Asn Leu
209 260 265 270
211 Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys Thr Cys Asn Val Thr
212 275 280 285

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214 Lys Gln Glu Cys Lys Lys Ile His Cys Pro Asn Arg Tyr Pro Cys Lys
215      290      295      300
217 Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys Val Cys Pro Gly Lys
218 305      310      315      320
220 Lys Ala Lys Gly Ala Leu Ala Gly Gly Pro Ala Phe Gly
221      325      330
224 <210> SEQ ID NO: 3
225 <211> LENGTH: 311
226 <212> TYPE: PRT
227 <213> ORGANISM: Mus musculus
229 <400> SEQUENCE: 3
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231 1      5      10      15
233 Tyr Arg Val Gly Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu
234      20      25      30
236 Val Tyr Cys Val Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys
237      35      40      45
239 Ser Arg Val Arg Cys Pro Ser Leu His Cys Leu Ser Pro Val His Ile
240      50      55      60
242 Pro His Leu Cys Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn
243 65      70      75      80
245 Asn Lys Val Thr Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln
246      85      90      95
248 His Gly Glu Leu Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro
249      100      105      110
251 Asn Gln Cys Ser Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly
252      115      120      125
254 Leu Lys Thr Cys Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro
255      130      135      140
257 Asp Ser Cys Cys Arg Val Cys Arg Gly Asp Ala Glu Leu Ser Trp Glu
258 145      150      155      160
260 His Ala Asp Gly Asp Ile Phe Arg Gln Pro Ala Asn Arg Glu Ala Arg
261      165      170      175
263 His Ser Tyr Leu Arg Ser Pro Tyr Asp Pro Pro Pro Asn Arg Gln Ala
264      180      185      190
266 Gly Gly Leu Pro Arg Phe Pro Gly Ser Arg Ser His Arg Gly Ala Val
267      195      200      205
269 Ile Asp Ser Gln Gln Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn
270      210      215      220
272 Asn Lys His Lys His Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr
273 225      230      235      240
275 Ser His Gly Glu Ser Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val
276      245      250      255
278 Glu Cys Val Leu Cys Thr Cys Asn Val Thr Lys Gln Glu Cys Lys Lys
279      260      265      270
281 Ile His Cys Pro Asn Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp
282      275      280      285
284 Gly Lys Cys Cys Lys Val Cys Pro Gly Lys Lys Ala Lys Gly Ala Leu
285      290      295      300

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297 <221> NAME/KEY: CDS
298 <222> LOCATION: (142)..(1287)
300 <220> FEATURE:
301 <221> NAME/KEY: sig_peptide
302 <222> LOCATION: (142)..(207)
304 <400> SEQUENCE: 4
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307 ccagtgcceca gctttagccc accagtccta ggagtcctcg agctgcattt tycagtagct 120
309 caaaggagaa gagagtggaa a atg gaa ggc ata aaa tat atc gcc tcc ttg 171
310 Met Glu Gly Ile Lys Tyr Ile Ala Ser Leu
311 1 5 10
313 gtt ttc ttc ttt gtt ttc ctg gaa gca agc aaa aca gag cca gta aaa 219
314 Val Phe Phe Phe Val Phe Leu Glu Ala Ser Lys Thr Glu Pro Val Lys
315 15 20 25
317 cac tca gag aca tat tgc atg ttt caa gac aag aag tat aga gtt ggt 267
318 His Ser Glu Thr Tyr Cys Met Phe Gln Asp Lys Lys Tyr Arg Val Gly
319 30 35 40
321 gag aaa tgg cat ccc tac ctg gaa cca tat gga ctg gtt tac tgt gtg 315
322 Glu Lys Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val
323 45 50 55
325 aac tgc atc tgc tca gag aat ggg aat gtg ctt tgc agc cga gtc aga 363
326 Asn Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg
327 60 65 70
329 tgt cca act ctt cat tgc ctt tca ccc gtg cat att cct cat ctg tgt 411
330 Cys Pro Thr Leu His Cys Leu Ser Pro Val His Ile Pro His Leu Cys
331 75 80 85 90
333 tgc ccc cgt tgc cca gac tcc tta cca ccg atg aac aat aag gtg acc 459
334 Cys Pro Arg Cys Pro Asp Ser Leu Pro Pro Met Asn Asn Lys Val Thr
335 95 100 105
337 agc aag tcc tgc gaa tac aat ggg acc acc tac caa cac gga gag ctc 507
338 Ser Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu
339 110 115 120
341 ttc ata gct gaa ggg ctc ttt cag aac cgg cag ccc aat cag tgc agt 555
342 Phe Ile Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Ser
343 125 130 135
345 cag tgc agc tgc tgc gag ggg aat gtg tat tgt ggt ctc aag act tgc 603
346 Gln Cys Ser Cys Ser Glu Gly Asn Val Tyr Cys Gly Leu Lys Thr Cys
347 140 145 150
349 ccc aaa ctg acc tgt gca ttc cca gtc tct gtt cca gat tcc tgc tgc 651
350 Pro Lys Leu Thr Cys Ala Phe Pro Val Ser Val Pro Asp Ser Cys Cys
351 155 160 165 170
353 cga gta tgc aga ggg gat gga gaa tta tca tgg gaa cat tct gat gct 699

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VERIFICATION SUMMARY                      DATE: 12/14/2000  
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L:13 M:270 C: Current Application Number differs, Replaced Application Number  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date

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